

DRAFT - DRAFT

AGCCTCCTGA	GTAATGAGTG	GCCTGGCCG	GAGCAGGCAG	GGTGGCCGGA	GCCGTGTGGA	60
CCAGGAGGAG	CGCTTTCCAC	AGGGCCTGTG	GACGGGGGTG	GCTATGAGAT	CCTGCCCGA	120
AGAGCAGTAC	TGGGATCCTC	TGCTGGGTAC	CTGCATGTCC	TGAAAACCA	TTTGCAACCA	180
TCAGAGCCAG	CGCACCTGTG	CAGCCTCTG	CAGGTCACTC	AGCTGCCGCA	AGGAGCAACG	240
CAAGTTCTAT	GACCATCTCC	TGAGGGACTG	CATCAGCTGT	GCCTCCATCT	GTGGACAGCA	300
CCCTAACCAA	TGTGCATACT	TCTGTGAGAA	CAAGCTCAGG	AGCCCAGTGA	ACCTTCCACC	360
AGAGCTCAGG	AGACAGCCGA	GTGGAGAAGT	TGAAAACAAT	TCAGACAACT	CGGGAAGGTA	420
CCAAGGATTG	GAGCACAGAG	GCTCAGAACG	AAGTCCAGCT	CTCCCCGGGC	TGAAGCTGAG	480
TGCAGATCAG	GTGGCCCTGG	TCTACAGCAC	GCTGGGGCTC	TGCCTGTGTG	CCGTCCCTCG	540
CTGCTTCCTG	GTGGCGGTGG	CCTGCTTCCT	CAAGAAGAGG	GGGGATCCCT	GCTCCTGCCA	600
GCCCCGCTCA	AGGCCCCGTC	AAAGTCCGGC	CAAGTCTTCC	CAGGATCAAG	CGATGGAAGC	660
CGGCAGCCCT	GTGAGCACAT	CCCCCGAGCC	AGTGGAGACC	TGCAGCTTCT	GCTTCCCTGA	720
GTGCAAGGCG	CCCACGCAGG	AGAGCGCAGT	CACGCCCTGGG	ACCCCCGACC	CCACTTGTGC	780
TGGAAGGTGG	GGGTGCCACA	CCAGGACCAC	AGTCCTGCAG	CCTTCCCCAC	ACATCCCAGA	840
CAGTGGCTT	GGCATTTGTG	GTGTGCCCTGC	CCAGGAGGGG	GGCCCGAGGTG	CATAAAATGGG	900
GGTCAGGGAG	GGAAAGGAGG	AGGGAGAGAG	ATGGAGAGGA	GGGGAGAGAG	AAAGAGAGGT	960
GGGGAGAGGG	GAGAGAGATA	TGAGGGAGAGA	GAGACAGAGG	AGGCAGAAAG	GGAGAGAAAC	1020
AGAGGAGACA	GAGAGGGAGA	GAGAGACAGA	GGGAGAGAGA	GACAGAGGGG	AAGAGAGGCA	1080
GAGAGGGAAA	GAGGCAGAGA	AGGAAGAGA	CAGGCAGAGA	AGGAGAGAGG	CAGAGAGGG	1140
GAGAGGCAGA	GAGGGAGAGA	GGCAGAGAGA	CAGAGAGGGG	GAGAGGACA	GAGAGAGATA	1200
GAGCAGGGAGG	TCGGGGCACT	CTGAGTCCC	GTTCCCAAGTG	CAGCTGTAGG	TCGTCATCAC	1260
CTAACACAC	GTGCAATAAA	GTCCTCGTGC	CTGCTGCTCA	CAGCCCCCGA	GAGCCCTCC	1320
TCTCTGGAGAA	TAAAACCTTT	GGCAGCTGCC	CTTCCTCAAA	AAAAAAAAAA	AAAAAAA	1377

FIGURE 1A

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
 20 25 30
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
 275 280 285
 Gly Gly Pro Gly Ala
 290

FIGURE 1B

(start and stop codons are in bold type)

AGCAAGTTCA GCCTGGTTAA GTCCAAGCTG AATTCCGGTC AAAGTTCAAG
TAGTGATATG GATGACTCCA CAGAAAGGGA GCAGTCACGC CTTACTTCTT
GCCTTAAGAA AAGAGAAGAA ATGAAACTGA AGGAGTGTGT TTCCATCCTC
CCACGGAAAGG AAAGCCCCTC TGTCCGATCC TCCAAAGACG GAAAGCTGCT
GGCTGCAACC TTGCTGCTGG CACTGCTGTC TTGCTGCCTC ACGGTGGTGT
CTTCTTACCA GGTGGCCGCC CTGCAAGGGG ACCTGGCCAG CCTCCGGGCA
GAGCTGCAGG GCCACCCACGC GGAGAAAGCTG CCAGCAGGAG CAGGAGCCCC
CAAGGCCGGC CTGGAGGAAG CTCCAGCTGT CACCGCGGGGA CTGAAAATCT
TTGAACCACC AGCTCCAGGA GAAGGCAACT CCAGTCAGAA CAGCAGAAAT
AAGCGTGCCG TTCAGGGTCC AGAAGAAAACA GTCACTCAAG ACTGCTTGCA
ACTGATTGCA GACAGTGAAA CACCAACTAT ACAAAAAAGGA TCTTACACAT
TTGTTCCATG GCTTCTCAGC TTTAAAAGGG GAAGTGCCT AGAAGAAAAA
GAGAATAAAA TATTGGTCAA AGAAACTGGT TACTTTTTA TATATGGTCA
GGTTTATAT ACTGATAAGA CCTACGCCAT GGGACATCTA ATTTCAGAGGA
AGAAGGTCCA TGTCTTGGG GATGAATTGA GTCTGGTGAC TTTGTTTCGA
TGTATTCAAA ATATGCCTGA AACACTACCC AATAATTCCCT GCTATTCAAGC
TGGCATTGCA AAACTGGAAG AAGGAGATGA ACTCCAACCT GCAATACCAA
GAGAAAATGC ACAAAATATCA CTGGATGGAG ATGTCACATT TTTGGTGCA
TTGAAAATGC TGTG**ACCTAC** TTACACCATG TCTGTAGCTA TTTCCCTCCC
TTTCTCTGTA CCTCTAAGAA GAAAGAATCT AACTGAAAAT ACCAAAAAAA
AAAAAAAAAAA AAAAAAGATCT TTAATTAAGC GGCGCAAGC TTATTCCCTT
TAGTGAG

FIGURE 2A

Translation in relevant reading frame (3' 5'):

MDDSTEREQS RLTSLKKRE EMKLKECVSI LPRKESPSVR SSKDGKLLAA
TLLLALLSCC LTVVSFYQVA ALQGDLASLR AELQGHHAEK LPAGAGAPKA
GLEEAPAVTA GLKIFEPPAP GEGNSSQNSR NKRAVQGPEE TVTQDCLQLI
ADSETPTIQK GSYTFVPWLL SFKRGSALEE KENKILVKET GYFFIYGQVL
YTDKTYAMGH LIQRKKVHVF GDELSLVTLF RCIQNMPETL PNNSCYSAGI
AKLEEDELQ LAIPRENAQI SLDGDVTFFG ALKLL

FIGURE 2B

Translation in relevant reading frame (3' 5'):

MARRLWILSL LAVTLTVALA APSQKSKRRT SSDRMKQIED KIEEILSKIY
HIENEIARIK KLIGERTRSG NSSQNSRNKR AVQGPEETVT QDCLQLIADS
ETPTIQKGSY TFVPWLLSFK RGSALEEKEN KILVKETGYF FIYGQVLYTD
KTYAMGHLIQ RKKVHVGDE LSLVTLFRCI QNMPETLPNN SCYSAGIAKL
EEGDELQLAI PRENAQISLD GDVTFFGALK LL
(SEQ ID NO:3)

FIGURE 3

FEB2499B

1.02 M_r

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Plate Binding assay-NLLZ + HUTACIFC (Goat anti-human Fc) 1/6/99
25-FEB-99

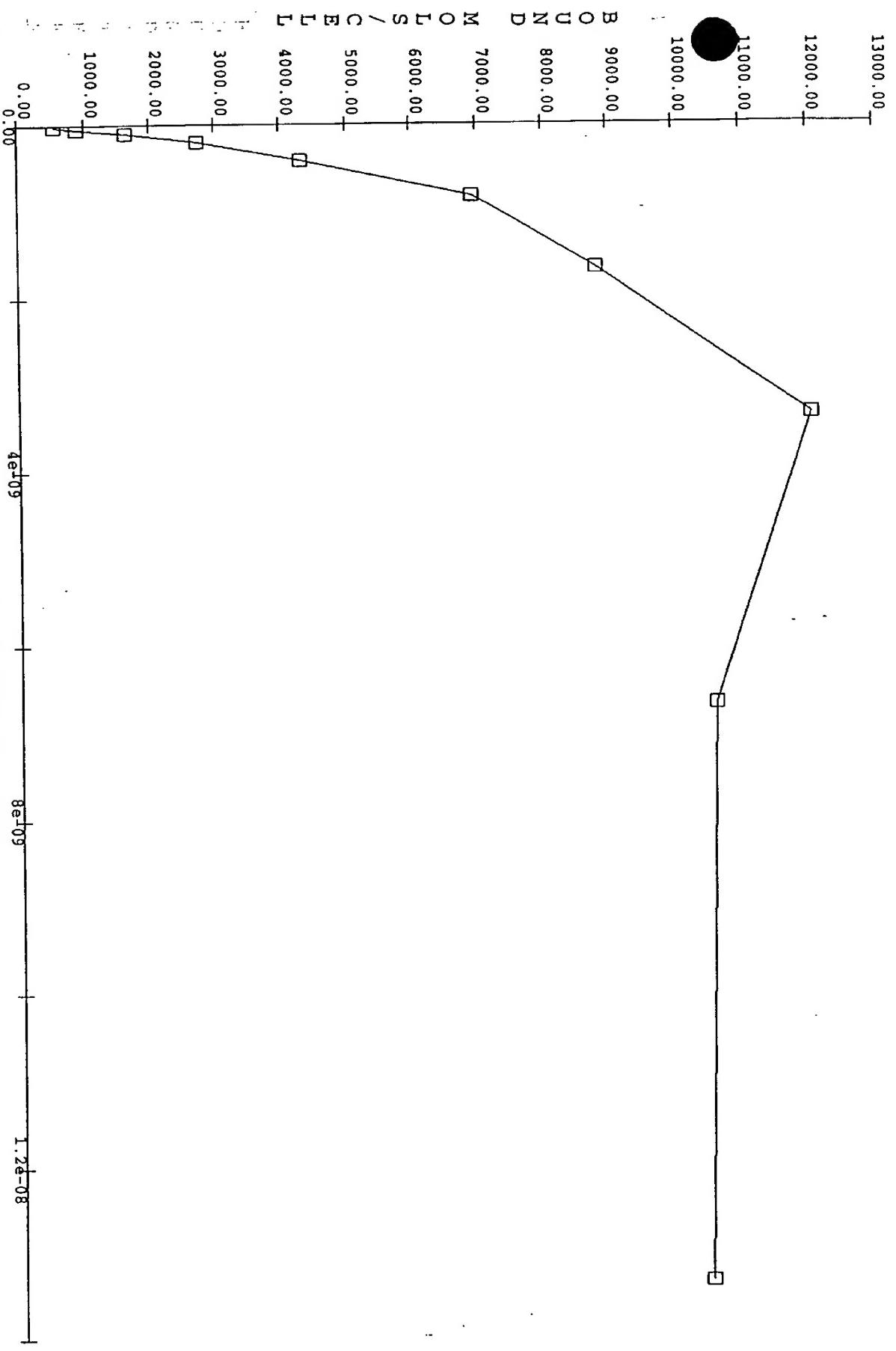


FIGURE 4A

FEB2499C

1; 2 d/h.
 Plate Binding assay-NLLZ + HutaCIFC (Goat anti-human Fc) 1/6/99
 25-FEB-99

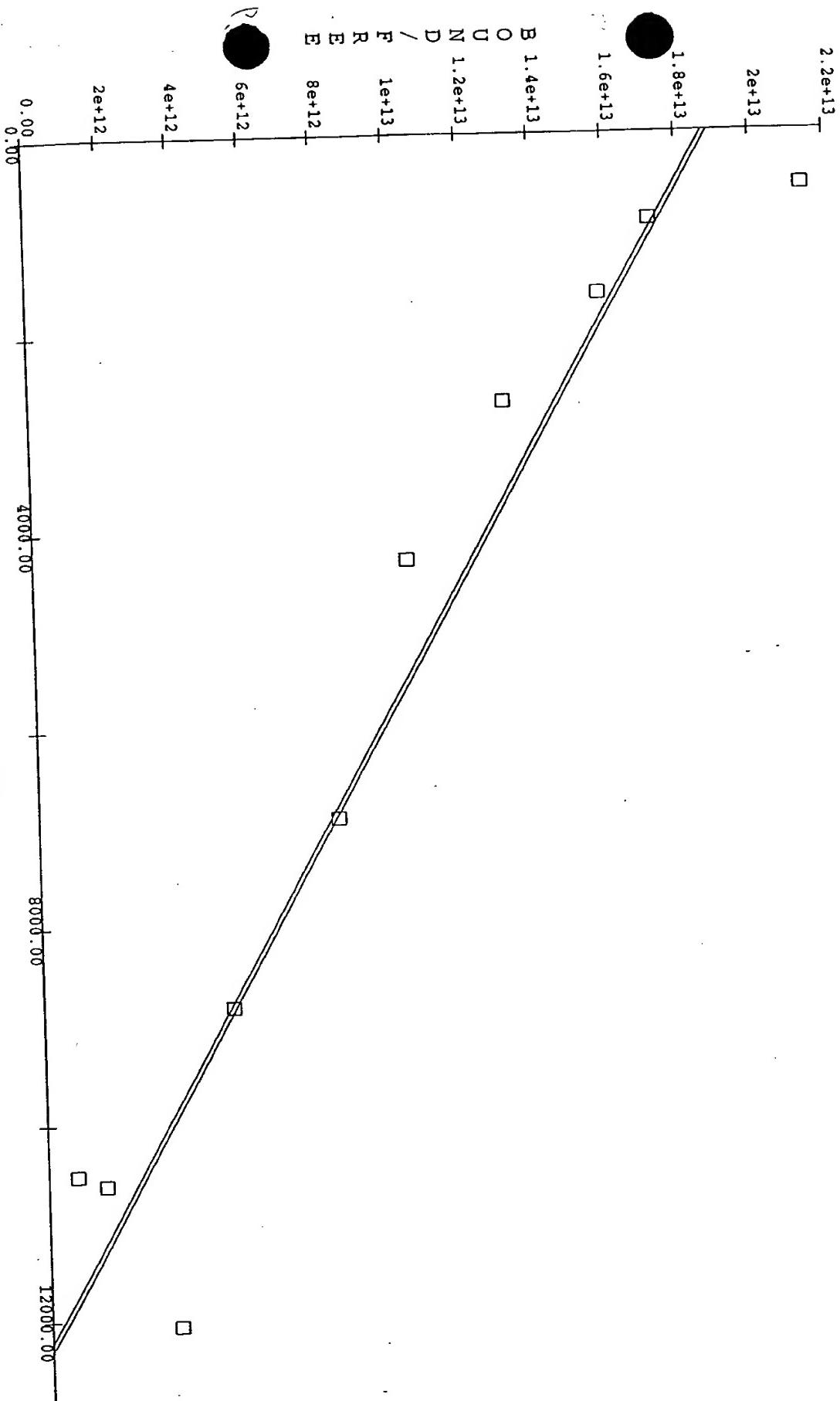


FIGURE 4B

CFEB2499C

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1:5 diln
Plate Binding assay-NLLZ + HUTACIFC (Goat anti-hu Fc) 1/6/99 duplicate
25-FEB-99

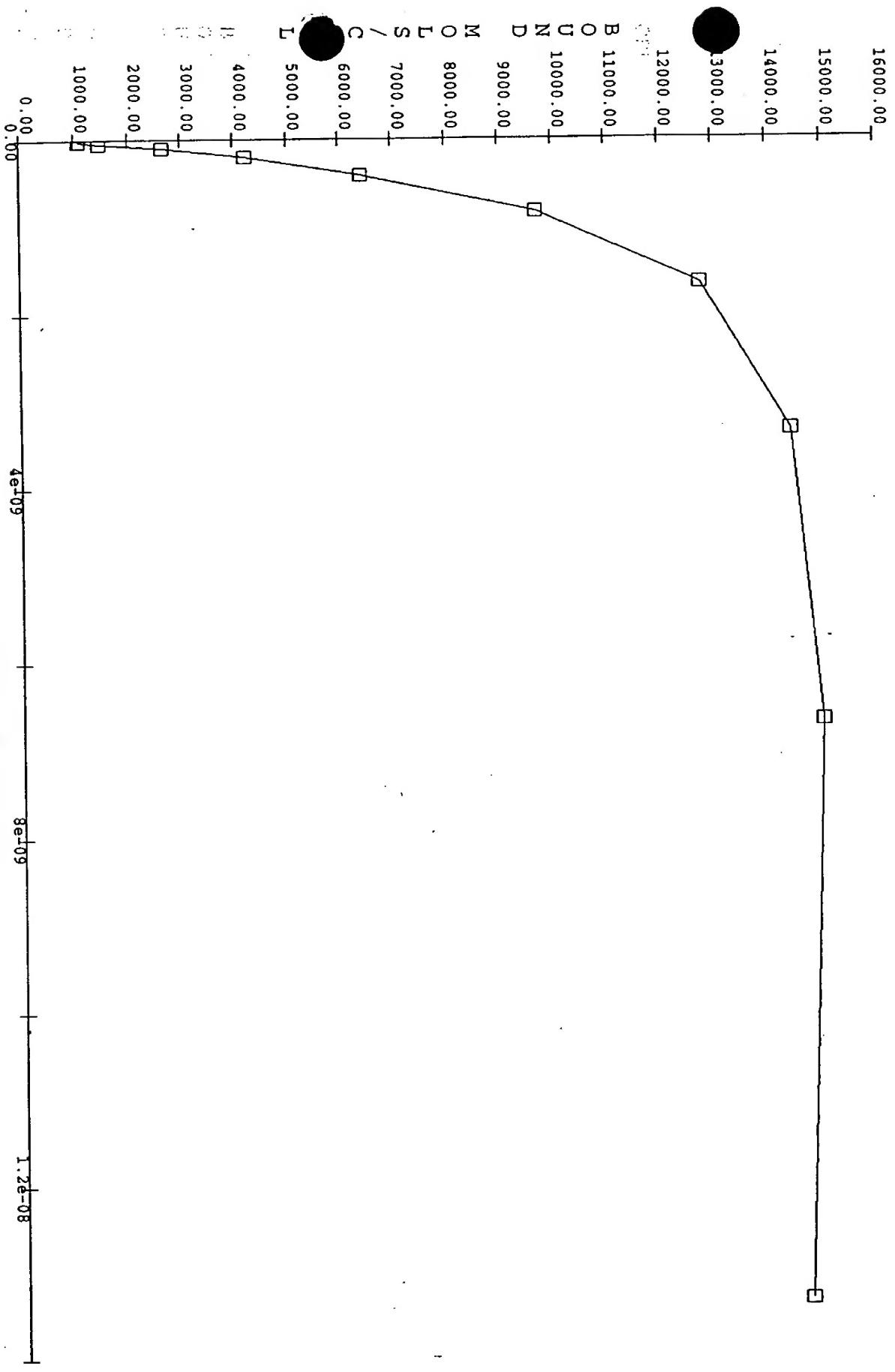


FIGURE 5A

Plate Binding assay-NLLZ + HUTACIFC (Goat anti-hu Fc) 1/6/99 duplicate
25-FEB-99

1:5 dil.

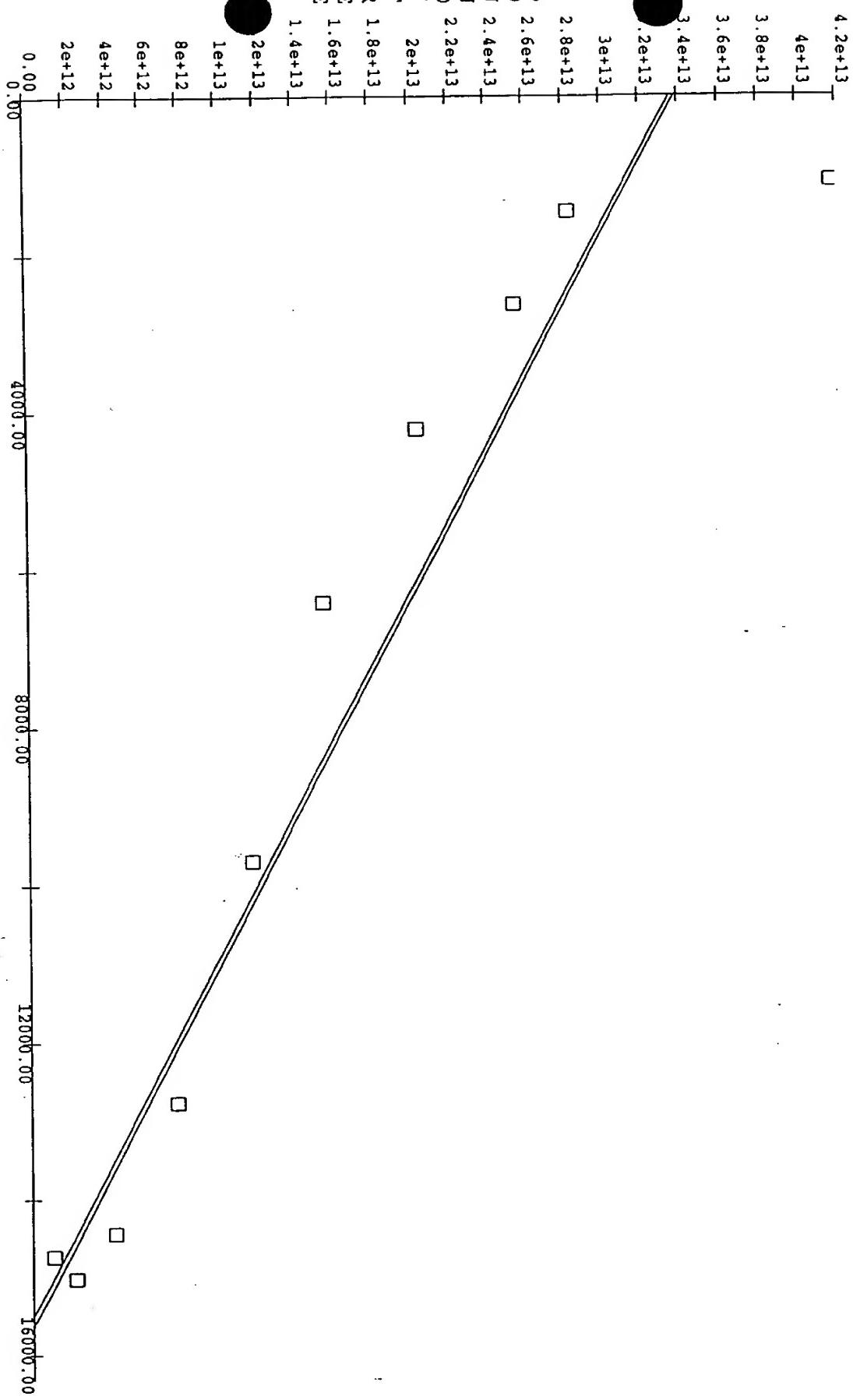
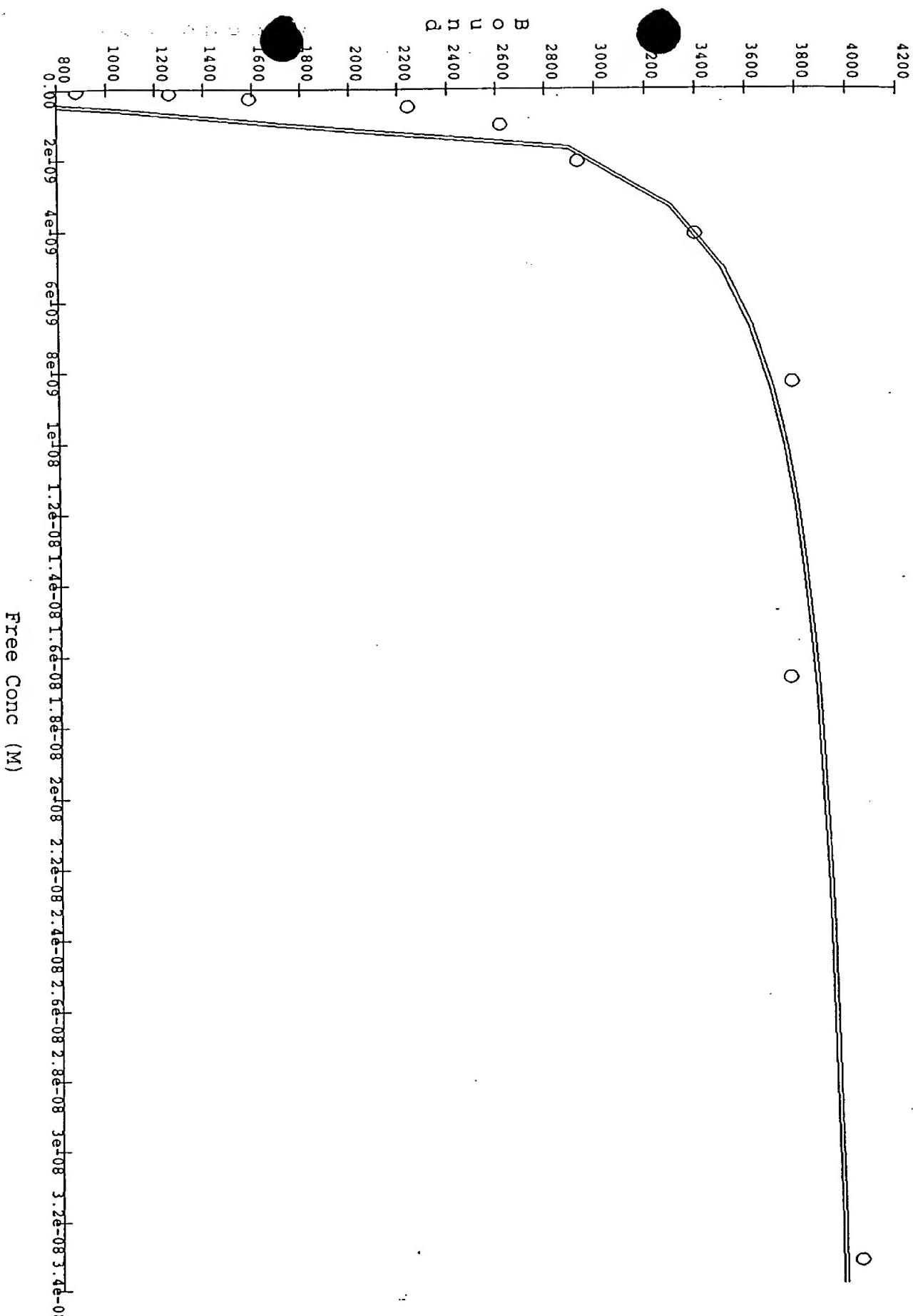


FIGURE 5B

125-I LZ M15 Plate Binding HUTACIFC (NLSN 1:10 11/10/98 td



\circ Data points
 $(2.1e+03 * 5.7e+08 * X) / (2.1e+03 * 7e+08 * X) + (1.9e+03 * 1.0e+10 * X) / (1 + 1.0e+10 * X)$

FIGURE 6A

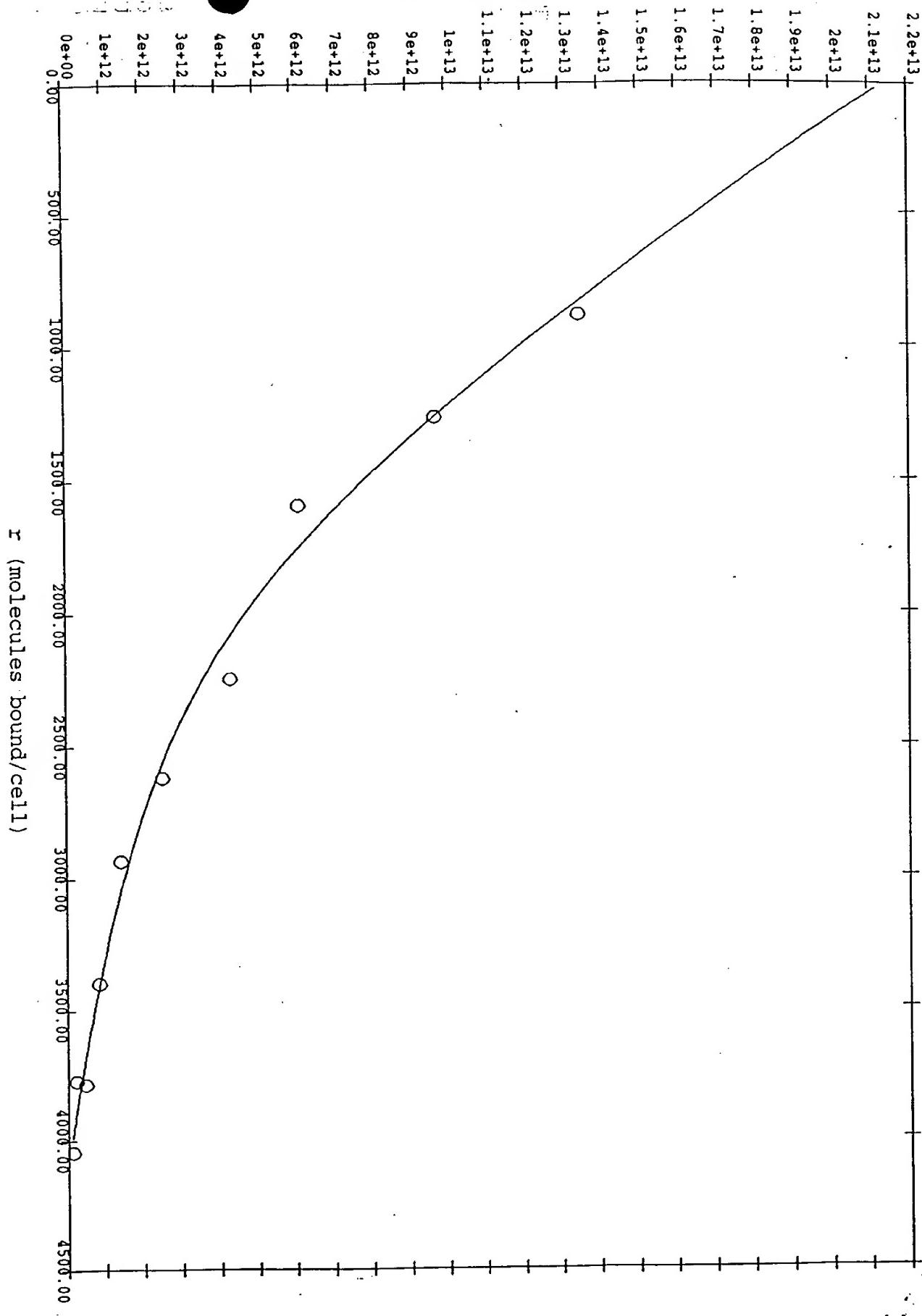


FIGURE 6B